



SEQUENCE LISTING

<110> Shaaltiel, Yoseph
<120> CELL/TISSUE CULTURING DEVICE, SYSTEM AND METHOD
<130> 27557
<160> 14
<170> PatentIn version 3.2
<210> 1
<211> 22
<212> PRT
<213> Artificial sequence
<220>
<223> Signal Peptide for the ER
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Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
1 5 10 15
Leu Ser Ser Ala Glu Phe
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<210> 2
<211> 7
<212> PRT
<213> Artificial sequence
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<223> Vacuolar targeting signal from Tobacco chitinase A
<400> 2
Asp Leu Leu Val Asp Thr Met
1 5
<210> 3
<211> 21
<212> DNA
<213> Artificial sequence
<220>
<223> Single strand DNA oligonucleotide
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cagaattcgc ccgccctgc a 21
<210> 4
<211> 22
<212> DNA
<213> Artificial sequence
<220>
<223> Single strand DNA oligonucleotide
<400> 4
ctcagatctt ggcgatgcc a 22
<210> 5
<211> 19
<212> DNA
<213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide

<400> 5
 ctcagaagac cagagggct 19

<210> 6
 <211> 17
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single strand DNA oligonucleotide

<400> 6
 caaagcggcc atcgtgc 17

<210> 7
 <211> 1491
 <212> DNA
 <213> Homo sapiens

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 gcccgcccct gcatccctaa aagcttcggc tacagctcgg tgggtgtgtg ctgcaatgcc 60
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 gagagtacac gcagtggcg acggatggag ctgagtatgg ggcccatcca ggctaatacac 180
 acgggcacag gcctgtact gaccctgcag ccagaacaga agttccagaa agtgaaggga 240
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1491

<210> 8
 <211> 497
 <212> PRT
 <213> Homo sapiens

<400> 8

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Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro
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Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg
 35 40 45

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
 50 55 60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
 65 70 75 80

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
 85 90 95

Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
 100 105 110

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe
 115 120 125

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu
 130 135 140

His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu
 145 150 155 160

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala
 165 170 175

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn
 180 185 190

Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr
 195 200 205

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys
 210 215 220

Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
 225 230 235 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
 245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
 260 265 270
 His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
 275 280 285
 Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr
 290 295 300
 Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala
 305 310 315 320
 Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
 325 330 335
 Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
 340 345 350
 Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
 355 360 365
 Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
 370 375 380
 Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
 385 390 395 400
 Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
 405 410 415
 Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
 420 425 430
 Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
 435 440 445
 Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
 450 455 460
 Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu
 465 470 475 480
 Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg
 485 490 495

Gln

<210> 9
 <211> 338
 <212> DNA
 <213> Artificial sequence
 <220>
 <223> CaMV 35S Promoter nucleic acid sequence

<400> 9
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 ggaaaggcta tcgttcaaga tgccctctacc gacagtggtc ccaaagatgg acccccaccc 180
 acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga 240
 tgtgatattc ccactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct 300
 tcctctatat aaggaagttc atttcatttg gagaggac 338

<210> 10
 <211> 66
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding the ER signal peptide

<400> 10
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 gaattc 66

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid sequence encoding the vacuolar targeting sequence

<400> 11
 gatcttttag tcgatactat g 21

<210> 12
 <211> 167
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Sequence for terminator

<220>
 <221> misc_feature
 <222> (162)..(162)
 <223> n is a, c, g, or t

<400> 12
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 agttaatgtg tgaatgtgtg aatgtgtgat tgtgacctga agggatcacg actataatcg 120
 tttataataa acaaagactt tgtcccaaaa accccccccc cngcaga 167

<210> 13
 <211> 2186
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic acid encoding recombinant GCD fused to signal peptides

<220>
 <221> misc_feature

<222> (2181)..(2181)

<223> n is a, c, g, or t

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ggaaaggcta tcgttcaaga tgccctctacc gacagtgggc ccaaagatgg acccccaccc	180
acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga	240
tgtgatatct ccactgacgt aagggatgac gcacaatccc actatccttc gcaagacctt	300
tcctctatat aaggaagttc atttcatttg gagaggacag gcttcttgag atccttcaac	360
aattaccaac aacaacaac aacaacaac attacaatta ctatttacia ttacagtcca	420
gggatccaag gagatataac aatgaagact aatctttttc tctttctcat cttttcactt	480
ctcctatcat tatcctgggc cgaattcgcc cgcctctgca tccctaaaag cttcggctac	540
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atgtgtgatt gtgacctgaa gggatcacga ctataatcgt ttataataaa caaagacttt 2160

gtcccaaaaa ccccccccc ngcaga 2186

<210> 14

<211> 526

<212> PRT

<213> Artificial sequence

<220>

<223> Recombinant GCD fused to signal peptides

<400> 14

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
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Leu Ser Ser Ala Glu Phe Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly
20 25 30

Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe
35 40 45

Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser
50 55 60

Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala
65 70 75 80

Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys
85 90 95

Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala
100 105 110

Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys
115 120 125

Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro
130 135 140

Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr
145 150 155 160

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr
165 170 175

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg
180 185 190

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
195 200 205

Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly
210 215 220

Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp

225	230	235	240
Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn	245	250	255
Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly	260	265	270
Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro	275	280	285
Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp	290	295	300
Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp	305	310	315
Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu	325	330	335
Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu	340	345	350
Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys	355	360	365
Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln	370	375	380
Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp	385	390	395
Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val	405	410	415
Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr	420	425	430
Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe	435	440	445
Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn	450	455	460
Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val	465	470	475
Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp	485	490	495
Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His	500	505	510
Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met	515	520	525